2009

ASSESSING THE PERFORMANCE OF SAMPLING DESIGNS FOR MEASURING ABUNDANCE OF UNDERSTORY PLANTS AFTER FOREST RESTORATION

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By

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Bachelor of Arts, Environmental Studies, Binghamton University, Binghamton, NY 1997

Thesis

presented in partial fulfillment of the requirements

for the degree of

Master of Sciences

in Forestry

The University of Montana

Missoula, MT

Spring 2009

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Title: Assessing the performance of sampling designs for measuring abundance of understory plants after forest restoration

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Abstract

Accurate estimation of the responses of understory plants to natural and anthropogenic disturbance is essential for understanding efficacy and non-target effects of management and restoration activities. However, ability to assess changes in abundance of understory plants that result from disturbance may be hampered by inappropriate sampling methodologies. Conventional methods for sampling understory plants may be robust for common, well-distributed species, but may fail to adequately characterize the abundance of less-common species, which are often the taxa of management concern. I tested conventional and novel approaches to sampling understory plants to determine their efficacy (in terms of number of replicates and time required) for quantifying abundance of plants of varying frequency and spatial heterogeneity on three control and three thinned-and-burned treatment units located within the western Montana block of the Fire and Fire Surrogates Project (FFS) — a large-scale investigation of the effects of fuel-hazard reduction treatments on a variety of ecosystem components. In each treatment unit, I used four sampling methods (modified Whittaker plots, Daubenmire transects, point line intercept transects, and strip adaptive cluster sampling) to estimate the cover of 24 understory species that vary in abundance. Compared to Daubenmire and point line intercept transects, modified Whittaker plots estimated cover with the lowest variances and, consequently, for the majority (67%) of species required the smallest sample sizes to accurately measure cover. However, this greater sampling efficiency was offset by increased time required to sample. For species grouped by growth-form and for common species, all three conventional sampling designs (i.e. Daubenmire transects, modified Whittaker plots, and point line intercept transects) were capable of estimating cover with a 50% relative margin of error with reasonable sample sizes (3-36 plots or transects for growth-form groups; 8-14 for common species); however, increasing the precision to 25% relative margin of error required sampling sizes that may be logistically infeasible (11-143 plots or transects for growth-form groups; 28-54 for common species). In addition, all three designs required enormous sample sizes to estimate cover of non-native species as a group (29-60 plots or transects) and of individual less-common species (62-118 plots or transects), even with 50% relative margin of error. Strip adaptive cluster sampling was the only method tested that efficiently sampled less-common species: for *Cirsium arvense*, an invasive non-native plant, adaptive sampling required five times fewer replicates than needed for modified Whittaker plots and 20 times less than for Daubenmire or point line intercept transects. My findings suggest that conventional designs may not be effective for accurately estimating the abundance of newly establishing, non-native plants as a group or of the majority of forest understory plants, which are characterized by low abundance and spatial aggregation. Novel methods such as strip adaptive cluster sampling should be considered in investigations for which cover of these species is a primary response variable.

Keywords*: Adaptive cluster sampling, sampling design, understory vegetation.*

Acknowledgements

I wish to thank my graduate advisor, Cara R. Nelson, and graduate advising committee members, David Affleck and Ragan Callaway, for their helpful insights, involvement, and statistical advice. I am grateful to Haley Wiggins for assistance with field data collection and the staff at University of Montana's Lubrecht Experimental Forest for facilitating field work.

Table of Contents

Tables and Figures

Introduction

Ecologists and land managers devote a considerable amount of attention to measuring responses of understory plants to natural disturbances and management activities (e.g., Fulé et al. 2005, Halpern and Spies 1995, Kerns et al. 2006, Metlen and Fiedler 2006, Nelson et al. 2008). Their ability to adequately assess vegetation responses, however, is based on the capabilities of the sampling methods that they employ. Most conventional sampling methods were designed to classify vegetation types by effectively characterizing abundance of common species (Thompson 2004) in relatively homogenous environments (Barnett and Stohlgren 2003). Thus, they may be adequate for providing unbiased estimates of mean abundance of dominant species or grouped growth-forms (i.e. graminoids or forbs), but may not adequately estimate abundance of less-common, heterogeneously-distributed plants (those with low local abundances or clumped spatial patterns). These less-abundant species comprise the majority of the native flora in forest ecosystems and frequently are the species of greatest management concern (Korb et al. 2003). For instance, at early stages of invasion, non-native plants may occur at low frequency and be restricted to particular micro-habitats; however, it is during this time period that their detection may be most critical for effective management (Rejmanek 2000). Although increasing or maintaining the diversity and abundance of native plants and reducing abundance of, and invasion susceptibility to, non-native invasive taxa are primary objectives of forest restoration treatments (Metlen and Fiedler 2006, Wienk et al. 2004, SER International Science and Policy Working Group 2004), not enough attention has been devoted to assessing the efficacy of sampling methods for

measuring responses of understory plants to disturbance and management (but see Abella and Covington 2004, Korb et al. 2003).

Many plant communities are composed of relatively few dominant (i.e. high relative abundance) plants, with the majority of species occurring at low abundance (Abella and Covington 2004, Lyons et al. 2005, Stohlgren et al. 1998) and with heterogeneous spatial distributions (Goslee 2006, Greig-Smith 1983, Small and McCarthy 2003). The distribution of these less-common, spatially aggregated plants is driven by forest resources that occur unevenly within forest stands (Barbier 2008, Halpern and Spies 1995), such as light, water, and soil nutrients, which are all affected by within-stand heterogeneity in structure, composition, and abiotic conditions. For instance, understory light availability depends on the spatial arrangement and composition of canopy and subcanopy trees (Barbier 2008, Miller et al. 2002); thus, variation in tree density, height, composition, and canopy openness create a mosaic of understory light patterns (Canham et al. 1990, Moora et al. 2007, Scheller 2002). In addition, soil nutrients and moisture tend to be patchily distributed within forest stands (Miller et al. 2002); microhabitats adjacent to rotting logs may be abundant in soil nutrients and water, whereas adjacent areas may contain acidic soils with limited available nutrients, due to thick accumulation of conifer litter. Disturbances also add to heterogeneity in resources within forest stands. Stands that have been burned or thinned generally contain a mosaic of within-stand disturbance intensities (Baker et al. 2007, Fulé et al. 2004, Knapp and Keeley 2006, Turner et al. 1997); pockets of higher severity soil disturbance (Miyanishi and Johnson 2002), altered resource availability (Gundale et al. 2005, Gundale et al. 2006, Moora et al. 2007), and open canopies occur unevenly throughout the stand. Accordingly, patterns

in understory vegetation are driven by within-stand heterogeneity of resources. For instance, ruderal species, fire-adapted native species and non-native invasive species may be more abundant in forest openings and disturbed pockets (Fulé et al. 2005, Griffis et al. 2001, Kerns et al. 2006, Metlen and Fiedler 2006). In contrast, undisturbed pockets may serve as refugia for late-seral herbaceous plants (Knapp et al. 2007, Nelson and Halpern 2005, Turner et al. 1997). Selection of sampling designs must be based on the spatial structure and heterogeneity of the overall plant community or the species of management concern (Barnett and Stohlgren 2003, Goslee 2006). Designs that do not capture the patchy nature of less-common native or non-native invasive plants may not be the most appropriate measurement strategies for assessing responses to disturbance.

Conventional sampling designs (i.e. those commonly reported in the ecological literature or used by federal land management agencies [e.g., USDI 2003 and USDA FIA 2007]) as implemented may not adequately estimate abundance of less-common plants due to low within-stand replication and total area sampled and, consequently, limited plot distribution (Table 1). Given constraints in funding and sampling time, there are trade-offs between the size of sample plots, the total number of plots, and their distribution within the study stand. For example, methodologies that include large plots (e.g., modified-Whittaker) may be sufficient for characterizing species diversity, particularly at multiple spatial scales (Stohlgren et al. 1995, Stohlgren et al. 1998); however, because they are costly in terms of sampling time, plot replication is generally limited (Barnett and Stohlgren 2003). Consequently, plots are not well distributed, and species that are aggregated or occur at low abundance are likely to be missed or underrepresented. In addition, limited replication associated with time-intensive designs may result in low

statistical power for detecting differences in abundance of individual species. On the other hand, designs such as point line intercept that sample a very small area are relatively fast to employ (Abella and Covington 2004) and can allow for considerable replication. Highly replicated point line intercept plots have been shown to quantify total plant cover with greater precision than other designs (Floyd and Anderson 1987); however, they may not adequately characterize abundances of individual species, especially those that are uncommon, due to limited sampling area (Korb et al. 2003, Stohlgren et al. 1998).

Although the comparative performance of sampling strategies has received considerable attention in the literature (e.g., Abella and Covington 2004, Etchberger and Krausman 1997, Huebner 2007, Korb et al. 2003, Shuman and Ambrose 2003, Stohlgren et al. 1998), previous investigations have not identified designs that effectively characterize abundance (cover and frequency) of understory species that vary widely in abundance and spatial patterning (e.g., common plants versus those that are less common and spatially aggregated), nor have they assessed the relative efficiencies of sampling designs in terms of required sample sizes and time to sample. For instance, several studies have compared the performance of vegetation sampling methods under field conditions, but none have explicitly examined abundance of individual species using adequate replicates of each sampling design (e.g., Abella and Covington 2004, Korb et al. 2003, Stohlgren et al. 1998) (Table 2). In addition, previous studies have focused on common species, rather than those that occur at low cover or frequency. For example, Abella and Covington (2004) excluded species with frequencies less than 5% from their comparative analysis of contiguous quadrats and point line intercept for detecting changes in community

composition (species richness and frequency) resulting from restoration treatments. Finally, most previous investigators (e.g., Goslee 2006, Huebner 2007, Stohlgren et al. 1998) did not control for sampling time (but see Abella and Covington 2004, Korb et al. 2003); thus, interpretations about efficacy of methods are confounded with time devoted to each method.

I examined the performance of conventional and novel sampling designs for estimating abundance of species of varying abundance (cover and frequency) in forest stands with differing management histories. Specifically, I assessed the strengths and limitations of three conventional methods designed to measure multiple species simultaneously (Daubenmire transects, modified Whittaker plots, and point line intercept transects) and one method designed for measuring an individual target species (strip adaptive cluster sampling), in order to address the following questions:

1) Does performance of sampling design vary with within-stand environmental heterogeneity (variation in light and soil disturbance) or between environments (untreated versus thinned-and-burned stands)?

2) Do estimates of mean abundance (cover) of total vegetation and vegetation grouped by growth form (graminoid, forb, or shrub) or origin (native versus non-native) vary based on sampling design employed?; and do estimates of mean abundance (cover and frequency) of individual species vary based on sampling design employed?

3) Is there variation among designs in required sample sizes and time-to-sample for estimating mean cover of total vegetation, of vegetation grouped by growth form or origin, and of individual species?

4) Do designs perform differently for common versus less-common species?

Methods

Study Site ~ This study was conducted at University of Montana's 11,000-ha Lubrecht Experimental Forest in western Montana (47° N, 113° W). Mean annual temperature is 7°C, and mean annual precipitation is 55cm—nearly half falling as snow (Nimlos 1986). The Forest is one of 13 sites in the national Fire and Fire Surrogate (FFS) study, which was designed to experimentally evaluate the effects and efficacy of forest restoration treatments on numerous ecosystem variables including understory vegetation (Weatherspoon and McIver, 2000). Sample stands range from 1263 to1388 m elevation and are dominated by second-growth ponderosa pine (*Pinus ponderosa*), Douglas-fir (*Pseudotsuga menziesii*), with occasional western larch (*Larix occidentalis*) and lodgepole pine (*Pinus contorta*). Dominant understory graminoids include *Calamagrostis rubescens* and *Carex geyeri*, dominant shrubs include *Symphorocarpus albus*, *Mahonia repens*, and *Spirea betulifolia*, and dominant forbs include *Achillea millifolium*, *Antennaria* spp. *Arnica cordifolia*, and *Fragaria virginiana*.

As part of the FFS study, four 9-ha experimental treatments (untreated control, prescribed burning only, mechanical thinning only, and thinning & burning) were implemented within each of three study blocks (located 3 km apart) in the spring of 2002 (see Metlen and Fiedler [2006] for a description of experimental treatments and design). I sampled the FFS treatment units that had been both thinned and burned (i.e. two management entries;

n=3), as well as the untreated units (no management entries; *n*=3), in order to capture the greatest range in abundance of individual species, as disturbance intensity has been found to be both positively correlated with invasion by non-native plants (e.g., Dodson and Fiedler 2006, Fulé et al. 2002, Griffis et al. 2001) and negatively correlated with late-seral forbs (Nelson and Halpern 2005).

Field Sampling ~ During the summer of 2008 at each of the six stands, data were collected on 1) total vegetation cover, 2) individual species cover for 24 understory plants, 3) species richness, and 4) time required to collect data, using each of the following four sampling designs (Figure 1):

Point Line Intercept Transect (*n*=16/treatment unit) — The point line intercept method is commonly used by federal agencies to sample understory cover (e.g., USDI 2003). Following National Park Service protocols, I sampled 50-m long transects, with points spaced every 30 cm (*n*=166 points/transect). At each point, a vertical projection was lowered, and the vegetation or substrate that was contacted was recorded. The proportion of points that intercept a particular species equals the cover of that species (Greig-Smith 1983). Advantages to this method include minimal observer bias (if both the line and points are made as dimensionless as possible) (Floyd and Anderson 1987) and relatively quick and simple application.

Daubenmire Transect (*n*=16/treatment unit) — Daubenmire transects (Daubenmire 1959) are widely used to estimate plant cover in a variety of ecological systems (e.g., Halpern et al. 2005, Nelson et al. 2008). Foliar cover is visually estimated by cover class, in systematically spaced quadrats along multiple transects. I used 50-m transects with 50 20 x 50-cm quadrats spaced every meter. Daubenmire transects are

relatively quick to sample, due to small subplot size. In addition, they allow for better representation of the stand if plots are well dispersed (Daubenmire 1959).

Modified Whittaker Plot (*n*=8/treatment unit) — Whittaker and modified Whittaker plots (Shmida 1984) have been advocated for measuring community diversity (Shmida 1984, Stohlgren et al. 1995), but are widely employed to measure both species richness and abundance of individual species. This design utilizes a 20 x 50-m multi-scale plot comprised of non-overlapping subplots. Within the 20 x 50-m plot, 10 1-m^2 quadrats are sampled for species richness and cover; in addition, species presence is recorded in two 10-m^2 subplots, one 100-m^2 subplot, and the full plot (see Stohlgren et al. [1995] for a complete description).

Strip Adaptive Cluster Sampling (SACS) (*n*=16 initial transects/treatment unit) — Adaptive sampling has been suggested to improve detection of species that are low in abundance and spatially aggregated (Brown 2003, Thompson 2002) (e.g., burgeoning invaders or less-common native plants). However, this method is infrequently reported in the plant ecology literature (but see Acharya et al. 2000, Philippi 2005). When a specified cover or density (the critical value) of a focal species is detected within a quadrat, additional quadrats are sampled surrounding the initial quadrat, thus allowing for better characterization of the clustering nature of species compared to that of non-adaptive designs. The number of adaptively added quadrats that are sampled will vary, according to rate of detection of particular species. SACS has the potential to compliment conventional sampling designs by efficiently detecting early non-native invasion and rare or less-common native species. In this investigation, I used a contiguous transect of 50 1 x 1-m quadrats (i.e. 1 x 50-m belt) as the first

phase of SACS sampling (Thompson 1991). For each 1-m^2 quadrat along the 50-m transect in which a target species was detected at or above the critical value, the four 1-m^2 quadrats that directly bordered the sampled quadrat were added to the sampling area for that target species (i.e. adaptively added neighborhoods consisted of four 1-m^2 quadrats in a cross pattern; Figure 1d). Successive quadrats were sampled using the same neighborhood rules, until the target species was not found at the critical value. Prior to data collection, I selected for sampling with SACS four target species with low abundances and patchy distributions (Table 3). I tested each of the four species using various size quadrats (ranging from 0.25-m^2 to 4-m^2) and critical detection values and variables (including species presence, densities, and percent cover). For each species, I subjectively selected response variable, critical value, and quadrat size, based on feasibility and sampling efficiency during these field trials.

In order to allocate similar amounts of time to each sampling design, I sampled half as many replicates for modified Whittaker plots (which are time consumptive to measure) on each treatment unit as I did for the faster-to-sample transect-based designs (point line intercept, Daubenmire and SACS). Because of the substantial amount of time required for initial set up of modified Whittaker plots, I sampled plots already established by the FSS study (Metlen and Fiedler 2006). Of the 10 FFS plots, I randomly selected seven to sample (Figure 2); in addition to these seven, I installed (and sampled) one additional modified Whittaker plot per treatment unit, in order to determine plot-establishment time (i.e. n=8 modified-Whittaker plots/treatment).

In order to minimize variation in sampling locations among designs, the three methods that involved transect sampling (point line intercept, Daubenmire, and SACS) were

located along one 50-m side of the modified Whittaker plots (Figure 2). Thus, sampling locations for each design were as similar to the other designs as possible. As mentioned above, Daubenmire, point line intercept, and SACS transects were sampled at twice the intensity of modified Whittaker plots because they are substantially quicker to sample and install. The eight transects for each design that were not located along the side of modified Whittaker plots were located using methods similar to those used to locate the FFS modified Whittaker plots (Metlen and Fiedler, 2006). Transect azimuths were consistent with Metlen and Fiedler (2006). Transect centers were randomly located within six systematically spaced rows along the length of the treatment unit, and randomly located anywhere along the 300-m width of the treatment unit (as opposed to within six systematically spaced columns). Transects were not permitted to overlap with previously established transects.

Twenty-four focal plant species, representing a range of origins, abundances, and distribution patterns, were selected for abundance measurements based on observed distributions at the study sites (Metlen et al. 2006) (Table 4). After identifying a suitable initial list of species, I subjectively selected species, preferentially including those that are of management concern, including invasive non-natives and late-seral forbs. Eight of the species were included because they occur on one or more state-level noxious weed lists in the Northwestern United States (Wyoming, Montana, Idaho, Washington or Oregon) (USDA plants database 2008) or due to potential for extensive ecological damage (e.g., *Bromus tectorum*; D'Antonio and Vitousek 1992).

Total vegetative cover, as well as cover and frequency of the 24 focal species, were collected using the three methods designed to measure multiple species (Daubenmire transect, and modified Whittaker plot, and point line intercept transect designs). I also used SACS to measure two native and two non-native species that show highly clustered distributions (Table 3), with each species sampled separately. The species measured by SACS were selected during pilot sampling at the beginning of the field season.

All data were collected between June 5 and August 3, 2008, after plants had fully leafed out and before late-summer desiccation began. The order that sites were sampled, as well as the order of sampling methods at each site, was random. The resolution for ocular estimates of percent cover was nearest 0.1% for values less than 1%, 1% for values between 1 and 10% and 5% for values greater than 10%. Narrow cover classes facilitate estimation of abundance of species that have low cover (Stohlgren et al. 1998) and do not overestimate low-cover species by using (high) midpoints of cover classes. To reduce observer error and bias (Kennedy and Addison 1987, Kercher et al. 2003), data were collected by only two individuals. Both were well trained using cover estimation guides, and estimations between observers were calibrated prior to the initial sampling period and regularly throughout the field season. In addition to collecting vegetation data, observers recorded the amount of time spent sampling, including time spent traveling between plots, surveying plot borders, and estimating species cover. For each sampling design (i.e. plot/transect type), a comprehensive survey of all vascular plants was conducted on one randomly selected plot or transect per treatment unit; for this plot or transect, species cover was collected for all species (not just the 24 target species) in order to determine the time required to sample all vascular plants present on each plot type. Finally, to

determine variability in environmental conditions and degree of disturbance, canopy cover was measured at the center of each modified Whittaker plot or transect using a spherical densitometer and soil disturbance by ocular estimation of percent cover of exposed mineral soil.

Statistical Analysis ~ Prior to analysis, for each design and each stand I calculated mean cover for each of the 24 focal species, and for total vegetation and species grouped by growth form (graminoids, forbs, shrubs) and origin (native and non-native). Grouped vegetation variables (i.e. species grouped by growth form and origin) only included data for the relevant 24 focal species, not for the plant community overall. For Daubenmire, point line intercept, and modified Whittaker designs, mean cover was first calculated at the transect or plot level using subplot or intercept data; these transect- or plot-level data were then used to compute stand-level means and standard deviations for each design. For SACS, stand-level mean cover and variances for individual species were calculated using unbiased estimators (1 and 2) (Affleck unpublished):

$$y_{ij} = \frac{\sum (\text{cover value}_l)}{\text{size of network}_l} \quad (1)$$

For strip (i.e. transect) i, where i = 1, 2, 3 …16 and quadrat$_{ij}$, where j = 1, 2, 3…50, where l is the network to which quadrat$_{ij}$ belongs:

$$\hat{\mu}_i = \frac{1}{50}\sum_i y_{ij} \quad (2)$$

$$\hat{\mu} = \frac{1}{n}\sum \hat{\mu}_i \quad (3)$$

$$\widehat{var}(\hat{\mu}) = \left(\frac{N-n}{N}\right)\frac{s^2_{\hat{\mu}}}{n} \quad (4)$$

where, *n* is the number of strips per stand (16); and *N* is the number of possible strips per stand (300). Stand-level frequency was calculated for each of the 24 species for each designs as the percentage of transects or plots within a stand containing the focal species.

To determine whether untreated sites and sites that were thinned and burned differed in light and soil environment, independent t-tests (Ott and Longnecker 2001) were performed to test for between-environment differences in mean canopy cover and percent bare ground. Additionally, independent t-tests were performed to test whether cover and within-stand standard deviations of individual and grouped species differed by environment, with separate tests for each variable and sampling design combination. Finally, to determine if overstory canopy cover or bare ground were significantly related to species cover, I conducted Pearson's correlations between individual or grouped vegetation cover and overstory canopy cover and bare ground.

Statistical tests for among-sampling-design differences in species cover were not possible, due to unequal variances among designs. However, effects of sampling design, environment (treated versus control), and their interaction on within-stand standard deviations of measurements of cover were assessed using split plot analysis of variance (ANOVA) models (Ott and Longnecker 2001), with sampling design and environment as fixed effects and forest stand and geographic block as random effects. Separate tests were performed for total vegetation, grouped vegetation variables derived from the 24 focal species (graminoids, forbs, shrubs and native and non-native plants), and each of the 24

focal species that met the assumptions of ANOVA. To correct for heteroscedasticity, values of within-stand standard deviations of individual species and grouped vegetation variables were log-transformed. In addition, split plot ANOVAs with Tukey's HSD post-hoc comparisons (Ott and Longnecker 2001) were used to determine whether sampling designs differ in total amount of time-to-sample one plot (which included time to establish and take down the plot, sampling time, and travel time between plots).

To assess differences among designs in requirements for replication and time-to-sample, I calculated the sample size necessary for each design to be within various margins of error with 90% confidence, using the formula:

$$n_k = \left[\frac{z_{0.05} * s_k}{E}\right]^2 \quad (5)$$

where, n_k is the required sample size for design k; $Z_{0.05}$ = 1.645 is the 5th percentile of the standard normal distribution, s_k is the estimated within-stand standard deviation of design k, and E is the margin of error. I calculated the above function for a range of E values. In addition, I also determined the sample sizes needed to achieve margins of error within 25% and 50% of the observed means (hereafter, relative margin of error or relative MoE):

$$n_{k,0.25} = \left[\frac{z_{0.05} * {}^{s_k}/_{\bar{x}_k}}{0.25}\right]^2 \quad (6a)$$

and

$$n_{k,05} = \left[\frac{z_{0.05} * {}^{s_k}/_{\bar{x}_k}}{0.5}\right]^2 \quad (6b)$$

where $\overline{x_k}$ is the estimated mean cover for design *k*.

For each design, I first determined required sample sizes independently for each stand on which the species was present and then averaged the resulting values. When sampling designs failed to detect a species within a particular stand (i.e. mean cover and standard deviation = 0), that stand was eliminated from sample size calculations for that particular sampling design. Sample size calculations were done for each species, grouped vegetation variable, grouped common species (the seven species that were present on all six stands and detected with all three multi-species sampling designs, and generally had cover estimates greater that 1%), and grouped less-common species (the 17 species that were not detected on all six stands by all three multi-species sampling designs). I determined time-to-sample requirements for each design by multiplying mean required sample sizes by the mean sampling time observed for that design.

All statistical analyses except sample size calculations were conducted using SPSS version 15.0 (SPSS Inc., Chicago, IL). Calculations of sample size and time-to-sample were done within Microsoft Excel 2007.

Results

Effect of environmental differences on species abundance and performance of sampling designs

There were significant differences between untreated sites and sites that were thinned and burned both in overstory canopy cover and in bare ground exposure (Figure 3a and b). Untreated stands had higher mean canopy cover (75 vs. 39%, respectively; $p<0.001$) and lower variability in canopy cover (average within-stand standard deviation of 9.49% vs. 16.18%, respectively; $p=0.004$). Although cover of bare ground was higher ($p<0.001$) on treated stands than on controls, the magnitude of this difference was low (0.12%, vs. 0.60% respectively). Untreated stands had significantly ($p=0.01$) less variability in exposed bare ground (average within-stand standard deviation of 0.28%, compared to 0.82% on treated stands).

While mean and within-stand variability in canopy cover and exposed bare ground differed between environments (treated vs. control), these variables were not significantly correlated with any grouped vegetation variable. Five of the 24 species, however, were detected only in stands that were treated: *Cirsium arvense*, *Cirsium vulgare*, *Cynoglossum officinale*, *Osmorhiza berteroi*, and *Potentilla glandulosa*. Another seven species were detected in only one control stand (Appendix 1). Of the 12 species that were commonly found in both environments, there were no significant differences in cover between environments. Of 54 tests performed (18 response variables [12 species and 6 grouped vegetation variables] and 3 designs), the only variable that showed a significant difference between the two environments was total vegetation cover ($p=0.033$, Daubenmire; $p=0.043$, modified Whittaker; and $p=0.18$ point line intercept). Similarly, there were few significant differences in within-stand standard deviations of grouped vegetation variables or individual species between the treated and control stands. The only variables that showed a significant between-environment difference in estimated

standard deviation were cover of total vegetation (p=0.051, point line intercept) and of native species (p=0.031, modified Whittaker; and p=0.021, point line intercept).

Among-design differences in abundance and sampling time

For grouped vegetation variables, mean cover and standard deviation estimates were always higher for point line intercept transects than the other two multi-species designs (Figure 4). This trend was particularly prominent for graminoid species: graminoid cover and associated standard deviations were five times greater using point line intercept than using the other two designs. For individual common species, point line intercept transects also produced the highest cover and within-stand standard deviation estimates (Figure 5, a and b). Daubenmire transects and modified Whittaker plots yielded cover and standard deviation values that were similar to each other.

For less-common species, differences among the three multi-species designs (Daubenmire, modified Whittaker, and point line intercept) could not be detected (Figure 5). However, coefficients of variations for all four less-common species were lower when sampled with SACS than when sampled with other designs (Figure 6, c). While mean cover estimates were similar when sampled with SACS, the within-stand standard deviation of the mean was always lower for SACS than the three multi-species designs (Figure 6, a and b).

As expected, the frequency (% of plots or transects within a stand on which species occurred) of individual species was consistently highest for modified Whittaker plots (1000-m^2), followed by Daubenmire transects and point line intercept transects,

respectively (Figure 7). While all multi-species designs detected all common species within all six stands, the sampling designs differed in their capacity to detect occurrence of less-common species (Figure 8). Modified Whittaker plots (1000-m^2) and Daubenmire transects detected the less-common species in more stands (4.3 and 3.4, respectively) than did the modified Whittaker 1-m^2 and 10-$m^{2)}$ subplots, and point line intercept transects (2.1, 2.4, and 2.0 stands, respectively) (p=0.057). Not surprisingly, modified Whittaker plots also averaged the highest species richness per plot, followed by Daubenmire and point line intercept transects (57, 28, and 15 species/plot or transect, respectively).

Time to sample one plot differed (p<0.001) by sampling design. For a two-person team to establish, sample (all species), and travel to one plot, Daubenmire transects required on average 135 minutes (128 excluding initial establishment, but including set-up and travel time), modified Whittaker plots 255 minutes (195 excluding initial establishment), and point line intercept transects 52 minutes (46 excluding initial establishment). A two-person team required on average 44 minutes to establish, sample (one individual species), and travel to one transect using SACS (38 excluding initial establishment).

Required Sampling Effort

For grouped vegetation variables, point line intercept transects required greater sample sizes than did modified Whittaker plots or Daubenmire transects to estimate mean cover within various margins of error (Figure 9a-c). However, modified Whittaker was the most time-intensive design (Figure 9d-f; Table 4) for all grouped variables; the required time-to-sample was similar using point line intercept and Daubenmire transects for all

variables except non-native cover, for which point line intercept was the least time-intensive design (Figure 9d-f; Table 4)

For individual species, point line intercept transects required greater sample sizes than modified Whittaker plots and Daubenmire transects to estimate mean cover to within various margins of error (Figure 10a-c). However, to estimate mean cover within 50% or 25% of the observed mean (i.e. relative margin of error), sample-size requirements varied among designs (because relative margin of error is based on observed mean cover, which varied within a species by design): for a 50% relative margin of error, point line intercept transects required the largest sample size for 46% of the 24 species sampled, modified Whittaker plots required the smallest sample size for 67% of the species, and Daubenmire transects required intermediate sample sizes (Table 4). For 63% of species, the increased precision of modified Whittaker plots was offset by the longer sampling time required (Table 4). On the other hand, for 88% of species the greater sample size required by point line intercept transects was offset by the shortest sampling time. Daubenmire transects required a shorter sampling time than modified Whittaker plots and a longer sampling time than point line intercept transects for 58% of the species.

When considering only common species, the modified Whittaker design required the fewest plots on average followed by Daubenmire and point line intercept designs (8, 9, 14 plots or transects/stand, respectively) to estimate cover within 50% of the observed mean with 90% confidence (Table 5). Conversely, for the same level of precision, the point line intercept design required the least amount of time to estimate cover of common species, followed by Daubenmire and modified Whittaker designs (12, 31, and 19 hr.,

respectively). For less-common species, the modified Whittaker design required the fewest plots on average, followed by point line intercept and Daubenmire designs (62, 75, 118 plots or transects/stand, respectively), to estimate cover within 50% of the observed mean with 90% confidence (Table 5). Again, the point line intercept design required least amount of time to estimate cover for less-common species within 50% of the observed mean, followed by modified Whittaker and Daubenmire methods (mean time-to-sample 61, 246, and 263 hr., respectively). Sampling using SACS produced enormous gains of efficiency in terms of sample size required to estimate cover within 50% or 25% of the estimated mean, for all four species sampled using this design (Table 4). SACS time-to-sample estimates are not directly comparable to multi-species designs because SACS was implemented separately for individual species rather than for multiple species simultaneously.

Discussion

There did not appear to be substantial differences in performance of sampling designs between environments (control versus thinned and burned stands). None of the three conventional designs showed significant between-environment differences in cover for any of the species that were abundant enough to be analyzed. Perhaps more importantly, I did not find between-environment differences in standard deviations of cover estimates for any species for any design. Also, the two grouped vegetation variables (total vegetation and natives) that had significant between-environment differences in standard deviations of cover estimates required similar sample sizes regardless of environment

(due to similar between-environment ratios of cover to standard deviation). Thus, the performance of sampling designs was not dependent on the post-treatment environment.

Among-design differences in abundance and variance

Sampling strategies intended to unbiasedly estimate mean cover of understory species varied in their efficiency for estimating plant cover. While expected cover estimates should be identical for all sampling designs (when coupled with associated unbiased estimators; Gregoire and Valentine 2008), I found that estimates of cover for common species differed appreciably among designs, suggesting large differences in precision. Point line intercept transects returned cover and standard deviation estimates that were up to five times larger than those of Daubenmire transects or modified Whittaker plots, with graminoids (individual species and as a group) showing largest the magnitude of difference. The higher values of vegetation cover (especially graminoid cover) that I observed with point line intercept transects is consistent with previous studies in forested (Korb et al. 2003) and grassland systems (Symstad et al. 2008). Plants with long, thin foliage (e.g., graminoid species) are more sensitive to measurement error caused by projection diameters greater than zero and non-vertical projections (Bonham 1989, Glatzle et al. 1993) and, consequently may be overestimated by point line intercept transects.

For less-common species, it was difficult to detect differences among the three conventional designs in standard deviations of cover estimates for less-common species, due to low cover estimates and variable occurrences among stands. However, SACS appears to be much more efficient than the three multi-species designs for estimating the

cover of these less-common, aggregated plants. SACS consistently produced the lowest estimated variances and for all four species the coefficients of variations and standard deviations obtained from SACS were always less than half that obtained from the other three designs.

I found substantial variation among designs in species' frequency (number of plots or transects containing focal species/stand) and constancy (number of stands containing focal species). Frequency was higher for designs with larger sample areas. Full modified Whittaker plots had higher within-stand frequencies of detection for all (common and uncommon) focal species, followed by Daubenmire and point line intercept transects. Although all designs had similar rates of constancy for common species, full modified Whittaker plots and Daubenmire transects had higher rates of constancy for less-common species than did the smaller modified Whittaker subplots and point line intercept transects. Point-line intercept had the lowest rates of both frequency and constancy for less-common plants, which I attribute to the small area sampled.

For quantifying plot-level species richness, designs with larger sampling areas, such as Modified Whittaker plots, out-performed designs with smaller sampling areas (e.g., Daubenmire and point line intercept transects). The modified Whittaker method resulted in twice as many species per plot as did Daubenmire transects and nearly four times as many species per plot as found using point line intercept transects. The point line intercept transects detected common species, but missed many less-common ones that were detected by Daubenmire transects and modified Whittaker plots. These results are consistent with multiple studies that suggest that large plot sizes may be necessary to

detect less-common species (Stohlgren et al. 1998, Korb et al. 2003, Symstad et al. 2008, Abella and Covington 2004). Furthermore, because designs that sample small areas consistently miss locally less-common species, they may underestimate species richness even if they are sampled with higher intensity (Barnett and Stohlgren 2003).

Sampling designs differed in the number of plots or transects required to accurately estimate cover of focal species. Although there was variation among individual species in which design required the smallest number of replicates, on average the modified Whittaker design required the smallest number of replicates to estimate cover with margin of errors within 50% of the observed mean, followed by Daubenmire transects, and then point line intercept transects.

For common species, all three conventional designs had achievable sample size requirements to estimate cover with a 50% relative margin of error, but none had attainable sample size requirements for achieving greater precision (e.g., 25% MoE). In addition, there were larger among-design differences in sample-size requirements associated with this greater precision: for instance, to estimate cover within 25% of the observed mean, point line intercept transects required nearly twice the sample size as modified Whittaker or Daubenmire designs.

For less-common species, all of the conventional designs required prohibitively high sample sizes (118, 62, and 75 Daubenmire transects, modified Whittaker plots, or point line intercept transects, respectively) to estimate cover even within a 50% relative margin of error. Similarly, to estimate the cover of grouped non-native plants to within 50% of

their observed mean required sample sizes of 60, 73, or 29 Daubenmire transects, modified Whittaker plots, or point line intercept transects, respectively. However, SACS dramatically reduced the sample sizes necessary to estimate cover to within 50% or 25% of the observed means, because of its low estimated standard deviations. For instance, the sample size required to estimate *Cirsium arvense,* an invasive non-native plant, was more than five times greater for modified Whittaker plots and 20 times greater for Daubenmire or point line intercept transects than it was for SACS. While sample size requirements were substantially lower for SACS, there must be sufficient replicates of SACS transects to ensure detection of the focal species. Consequently, the selection of sample sizes must consider both the estimated variances and detection capability.

The unequal number of stands included for sample size calculations complicates inference about the reliability of sample size estimates for less-common species. I calculated sample size requirements only from stands where the focal species were detected; including stands in which a focal species was not detected by a design in sample size calculations for that design would have resulted in standard deviations equal to zero and, consequently, sample-size requirements would be unrealistically low. However, this procedure may explain why point line intercept transects required smaller sample sizes than Daubenmire transects for less-common species. Point line intercept transects detected the less-common species in fewer stands than Daubenmire transects; thus, Daubenmire sample size calculations included stands with high variances in species cover that were excluded from point-line intercept sample-size analysis. For less-common species, the greater detection capability of Daubenmire transects may have biased sample-size requirements against this design.

Although sampling designs that employ ocular estimation of foliar cover (i.e. Daubenmire transects and modified Whittaker plots) required smaller sample sizes than point line intercept transects, point line intercept required the least time-to-sample for grouped vegetation variables, as well as for both common and less-common plants. The relatively fast time-to-sample with point line intercept transects more than compensated for the larger sample sizes they required to estimate mean cover, with the caveat that point-line intercept had low rates of species detection. Daubenmire transects required less time to accurately estimate cover of grouped vegetation variables and common species than modified Whittaker plots, while the modified Whittaker design required marginally less time to sample less-common focal species than did Daubenmire transects. While previous studies have not explicitly evaluated sampling efficiency with regard to sample size and associated time-to-sample, my results are consistent with previous investigations in ponderosa pine dominated forests (Korb et al. 2003, Abella and Covington 2004) and grassland ecosystems (Symstad et al. 2008) that have found point line intercept transects take significantly less time than designs that use ocular estimation.

In this study, time-to-sample one plot includes the times it takes to establish and remove the plot, sample all species, and travel to one plot. I found initial establishment time to be considerable for large, multi-scaled modified Whittaker plots (average of 80 minutes for two people: 107 minutes in untreated and 55 minutes in thinned-and-burned stands), whereas transect-based designs took on average only 14 minutes for two people to install. For investigations that require one-time measurements (e.g., this investigation), among-design differences in establishment design may be important to consider. However, this consideration may be less important for investigations that require repeated sampling

over long time frames, as the time it takes to establish the plots will only affect the first year of sampling.

Studies of the responses of understory plants to restoration treatments generally have sample sizes in the range of what is required to estimate the cover of common species to within 50% of their observed mean (on my 9-ha stands, 9, 8, or 14 Daubenmire transects, modified Whittaker plots, or point line intercept transects, respectively). However, the sample sizes required to accurately estimate cover of common species with greater precision (e.g., within 25% of the observed mean) are above what are commonly done (32, 28, 54 Daubenmire transects, modified Whittaker plots, or point line intercept transects, respectively). Similarly, species grouped by growth-form require achievable sample sizes to estimate cover within 50% of the observed means. Sample sizes required for greater precision (e.g., within 25% of the observed mean) also may be achievable, particularly for graminoids and forbs. Thus, if investigations are concerned only with abundances of common species or species grouped by growth-form, using sampling designs that are relatively quick to implement (i.e. point line intercept or Daubenmire transects) may be more efficient than more labor-intensive modified Whittaker plots. However, if estimating cover of less-common species is a goal, the only reliable design of the ones I tested was SACS.

Practical considerations when implementing SACS

This is one of the first field applications of adaptive cluster sampling for plant species (but see Acharya et al. 2000 and Phillippi 2005). The fact that SACS resulted in lower variances and greater sampling efficiency than other designs suggests that it may be a

promising method for understory plants that are locally rare and aggregated. However, there are several practical matters to consider when applying this design. The most obvious limitation is that SACS is meant for sampling one rather than multiple species and, therefore, can not be used to characterize plant community composition. Thus, species that warrant use of this design should be of management or scientific concern, such as highly invasive non-natives or rare natives. In addition, species sampled with SACS must have aggregated distributions in order to benefit from the adaptive nature of the design; there would be no gain in efficiency for species that do not show aggregated distributions (Thompson 2002, Brown 2003).

There are several other factors that must be taken into consideration prior to selecting an adaptive design, including the fact that the efficiency of the design is greatly affected by the selected critical value, adaptive network arrangement, arrangement of primary units, and unit (quadrat) size (Thompson 2002, Brown 2003). In this study, the adaptive criteria were determined by pilot sampling. For instance, while larger quadrat sizes could enhance sampling efficiency for some species, estimating cover of understory plants in quadrats greater than 1-m^2 could increase measurement error or be difficult to implement where trees and other vegetation are abundant. Another consideration when implementing this design for understory plants is the high potential for trampling the focal species and surrounding vegetation. As units are added to the initial strip (or neighborhood quadrats), the network expands outwards; thus, care must be taken not to trample plants that have not yet been sampled. Another drawback of adaptive sampling is that it is not possible to know in advance how long any one strip will take to sample. In this study, most strips did not contain the species of interest; thus, the sampling time was

frequently approximately ten minutes (not including set-up or travel time). Alternatively, sampling one particular strip for *Cirsium arvense* took a team of two nearly five hours. Finally, defining protocols (e.g., critical values, networks, shape of initial units) for adaptive sampling is inherently species and location specific; the lack of standard protocols makes this design more difficult to implement relative to conventional designs.

Conclusion

Selection of sampling strategies for understory plants must be driven by the specific research or sampling objectives, as there are no one-size-fits-all designs. A design that is most efficient for characterizing community composition (including diversity) may not be appropriate for estimating cover of individual species or species grouped by growth-form. While large, multi-scale designs, such as modified Whittaker plots may quantify species richness, these large and labor-intensive designs may not be the best approach for precisely estimating abundances of individual species. While all three multi-species sampling designs (Daubenmire transects, modified Whittaker plots, and point line intercept transects) were capable of estimating the cover of common species and species grouped by growth-form with reasonable sample sizes (albeit different time-to-sample), these designs require prohibitively high sample sizes to estimate cover of less-common species or non-native species as a group. This is especially troublesome, given that less-common species comprise the majority of the diversity in forested systems and are frequently of management concern, whether they be threatened or endangered or invasive non-native plants in the early stages of establishment. The low cover and relatively high variability of these species makes it difficult both to precisely estimate their cover and to

detect differences in cover among environments with different management histories. I found that sampling with SACS offers tremendous gains in precision for sampling individual target species, in comparison to multi-species designs. Consequently, if a primary research objective is to efficiently estimate the cover of individual less-common and aggregated species of concern, SACS may be the most appropriate sampling approach.

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Table 1. Description of commonly used sampling designs, including measurement method and total area sampled per transect or plot.

			Total area sampled	
Sampling design	Description	Measurement method	Cover ($m^{2)}$	Presence (m^2)
Daubenmire transects	50-m transect with 50 20 x 50-cm even-spaced quadrats	Ocular estimates of foliar cover using cover classes	5	5
Modified Whittaker plots	20 x 50-m plot (1000-m^2) with one 100-m^2, two 10-m^2, and 10 1-m^2 subplots	Species presence in 1000-m^2 plot; ocular estimates of foliar cover in 10 1-m^2 subplots.	10	1000
Point line intercept transects	50-m transect with 166 points	Foliar cover measured by plant interceptions	very limited	very limited

Table 2. Previous field-based comparative investigations of the efficacy of sampling designs. Numbers indicate replication of plots/experimental unit. Superscripts indicate significant differences among designs: a = design(s) with highest richness/plot; b = design(s) with highest richness/experimental unit; c = design with greatest total cover or frequency; and d = design with highest precision.

					Sampling design												
Variable	Author	Year	Vegetation type	Size of exp. units (ha)	Point line intercept	Line intercept	Strip transect	Belt	Daubenmire	Adaptations of Daubenmire	Parker Transect	Modified Whittaker	Small Modified Whittaker	100m^2 plot	Stratified multi-scale quadrats	Systematic quadrats
Richness																
	Abella & Covington	2004	Forest	14	32		32^{ab}									
	Barnett & Stohlgren	2003	Forest	10,000								8^{a}	15	28		
	Huebner C	2007	Forest	2								1			60^{b}	32
	Korb et al.	2003	Forest	16	20			8^{b}		10		4^{ab}				
	Prosser et al.	2003	Grassland	3,470	45					45^{b}						
	Stohlgren et al.	1998	Grassland	not stated					4	4	3	1^{ab}				
Cover																
	Floyd & Anderson	1987	Shrubland	not stated	163^{d}	163^{c}			163							
	Korb et al.	2003	Forest	16	20^{c}					10		4				
	Stohlgren et al.	1998	Grassland	not stated					4	4	3	1				
Frequency																
	Abella & Covington	2004	Forest	14	32		32^{c}									

Notes on sampling designs: *Point line intercept*– transect with plant cover measured at systematic points; *line intercept* – transect with distance of cover measured where plant intercepts the line; *strip transect* – 50-m transect with 50 1 x 1-m contiguous subplots; *belt* – 50m long x 10m wide; *Daubenmire* – 20 x 50-cm quadrats on first half of each meter along transect (with 6 cover classes); *Adaptations of Daubenmire* – various; *Parker transect* – 30.48-m transect with 100 x 1.9-cm diameter ring spaced every 30.5cm; *Modified Whittaker* – 20 x 50-m large plot with subplots (1 x 100m^2, 2 x 10m^2, 10 x 1m^2); *small Modified Whittaker* – 5 x 20-m plot with subplots (1 x 10m^2, 4 x 1m^2); *multi-scale quadrats* – 40 x 1-m^2 plots and 20 x 10-m^2 plots; *systematic quadrats* – 1-m^2 quadrats in systematic clusters along a 200-m transect.

Table 3. Species sampled with the strip adaptive cluster design, and the quadrat sizes, critical values, and response variables used for each.

Species	Quadrat size	Critical value	Response variable
Cirsium arvense	1-m^2	1 individual	Percent cover
Bromus tectorum	1-m^2	0.5% cover	Percent cover
Smilacina racemosa	1-m^2	1 individual	Percent cover
Heuchera cylindrica	1-m^2	1% cover	Percent cover

Table 4. For each sampling design (Daubenmire transect, D; modified Whittaker plot, M; point line intercept transect, P; and strip adaptive cluster sampling, S) observed mean cover and constancy (number of stands, range of 1-6) for grouped vegetation variables and individual species, and sample size (number of plots or transects) and time-to-sample (hr) required for estimation of mean cover within 50% and 25% of the observed mean. For cover < 0.005%, t indicates trace.

Species	Design	Cover (%)	Occurrence (#)	Sample size (#)		Time (hr)	
				50%	25%	50%	25%
Grouped vegetation variables							
Total vegetation	D	35.6	6	1	2	2	4
	M	36.02	6	1	4	4	17
	P	57.61	6	2	5	2	4
Forbs	D	6.52	6	10	38	22	85
	M	5.94	6	10	38	43	162
	P	8.81	6	36	143	31	124
Graminoids	D	4.62	6	4	16	9	36
	M	4.1	6	3	11	13	47
	P	22.63	6	4	16	3	14
Shrubs	D	10.17	6	3	12	7	27
	M	8.22	6	3	11	13	47
	P	13.28	6	4	15	3	13
Natives	D	20.8	6	2	7	4	16
	M	17.81	6	2	7	9	30
	P	43.93	6	3	9	3	8
Non-natives	D	0.61	5	60	240	135	539
	M	0.44	5	43	171	183	729
	P	1.58	3	29	113	25	98

Table 4 Continued

Species	Design	Cover (%)	Occurrence (#)	Sample size (#)		Time (hr)	
				50%	25%	50%	25%
Common Species							
Arnica cordifolia[1]	D	4.58	6	11	41	25	92
	M	4.34	6	10	39	43	166
	P	5.62	6	12	48	10	42
Calamagrostis rubescens[2]	D	3.3	6	7	28	16	63
	M	2.92	6	5	17	21	72
	P	16.97	6	6	24	5	21
Carex geyeri[2]	D	1.3	6	6	24	13	54
	M	1.18	6	6	24	26	102
	P	5.62	6	7	25	6	22
Fragaria virginiana[1]	D	0.56	6	10	37	22	83
	M	0.42	6	11	41	47	175
	P	1.07	6	27	105	23	91
Mahonia repens[3]	D	3.68	6	6	23	13	52
	M	3.03	6	3	12	13	51
	P	4.03	6	6	24	5	21
Penstemon alberti[1]	D	0.5	6	12	46	27	103
	M	0.48	6	11	43	47	183
	P	0.77	6	30	120	26	104
Symphoricarpos albus[3]	D	6.49	6	6	23	13	52
	M	5.19	6	5	20	21	85
	P	9.24	6	7	27	6	23

Table 4 Continued

Species	Design	Cover (%)	Occurrence (#)	Sample size (#) 50%	Sample size (#) 25%	Time (hr) 50%	Time (hr) 25%
Less-common species							
*Bromus tectorum**	D	*t*	4	249	993	560	2232
	M		0				
	P		0				
	S	0.01	1	11	43	8	31
Campanula rotundifolia[1]	D	0.02	5	146	583	328	1310
	M	0.06	1	59	234	252	998
	P	0.09	2	88	351	76	304
Carduus nutans[1]*	D	0.01	2	133	531	299	1193
	M	0.03	3	86	344	367	1467
	P	0.04	1	174	693	151	601
Centaurea maculosa[1]*	D	0.12	4	101	404	227	908
	M	0.04	4	79	313	337	1335
	P	0.4	3	67	267	58	231
Cirsium arvense[1]*	D	0.06	2	173	691	389	1553
	M	0.36	1	43	170	183	725
	P	0.04	1	174	693	151	601
	S	0.05	2	8	29	6	21
Cirsium vulgare[1]*	D	0.49	2	98	391	220	879
	M	0.3	2	2	109	9	465
	P	0.58	2	57	225	49	195
*Cynoglossum officinale**[1]	D	*t*	2	261	1042	587	2342
	M	0.01	1	79	316	337	1347
	P		0				

Table 4 Continued

Species	Design	Cover (%)	Occurrence (#)	Sample size (#)		Time (hr)	
				50%	25%	50%	25%
Heuchera cylindrica[1]	D	0.05	6	131	523	294	1175
	M	0.03	5	68	271	290	1156
	P	0.14	5	115	459	100	398
	S	0.05	6	1	4	1	3
Lithospermum ruderale[1]	D	0.06	2	63	249	142	560
	M	0.1	2	70	279	298	1190
	P	0.13	2	102	406	88	352
Luzula campestris[2]	D	0.02	4	69	276	155	620
	M	0.01	3	25	98	107	418
	P	0.15	2	58	231	50	200
Osmorhiza berteroi[1]	D	0.07	1	54	215	121	483
	M	0.06	1	32	128	136	546
	P	0.23	1	51	201	44	174
Potentilla glandulosa[1]	D	0.02	3	96	381	216	856
	M	*t*	1	79	316	337	1347
	P		0				
Potentilla gracilis[1]	D	0.37	3	48	191	108	429
	M	0.26	3	106	423	452	1804
	P	0.54	3	38	150	33	130
Potentilla recta[1]*	D	0.36	3	38	151	85	339
	M	0.13	4	35	140	149	597
	P	0.63	3	220	55	191	48

Table 4 Continued

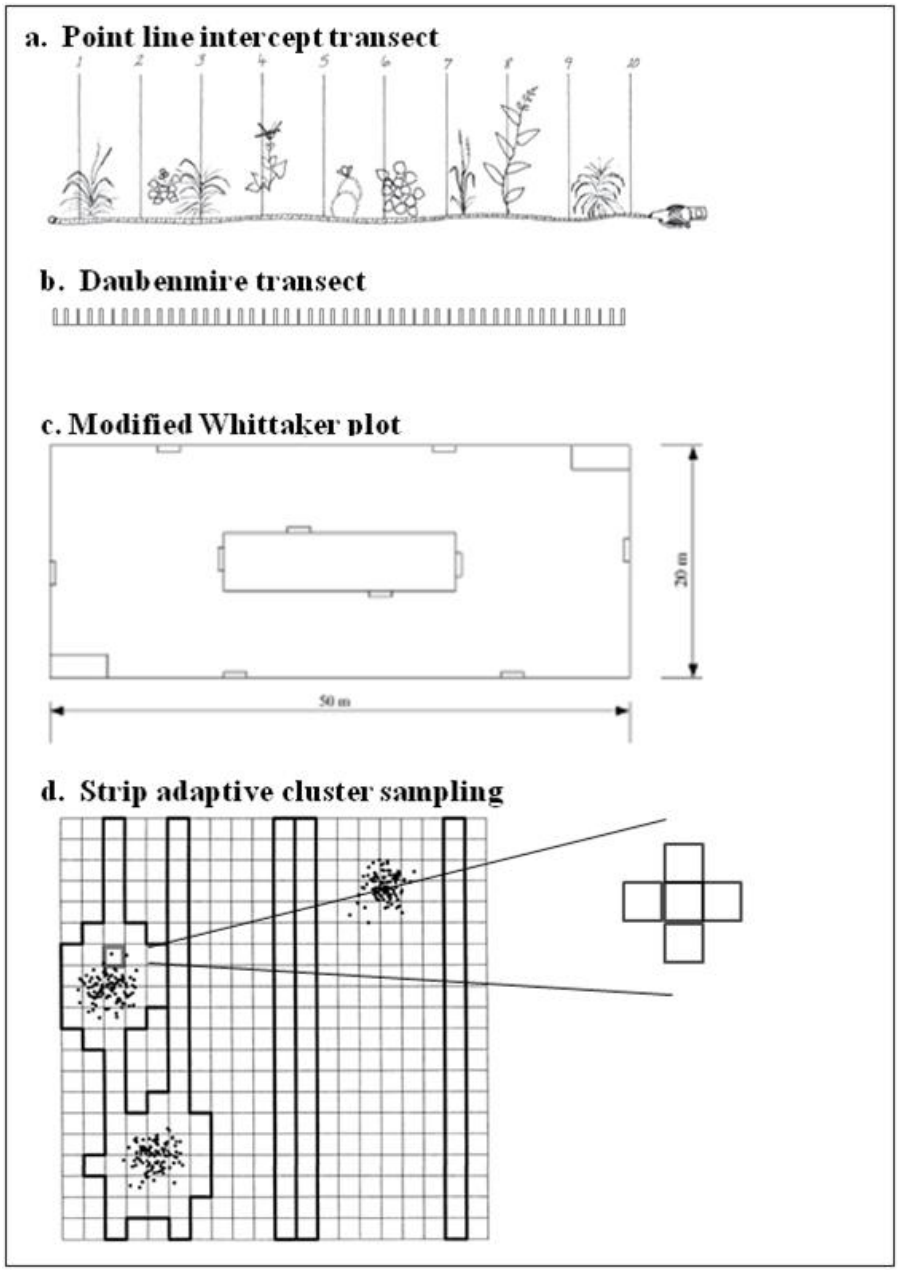
Species	Design	Cover (%)	Occurrence (#)	Sample size (#)		Time (hr)	
				50%	25%	50%	25%
Smilacina racemosa[1]	D	0.02	3	161	642	362	1443
	M	0.5	1	87	347	371	1480
	P	0.04	1	174	693	151	601
	S	0.01	3	8	30	6	22
Valeriana dioica[1]	D	0.03	5	71	283	160	636
	M	0.04	4	42	168	179	716
	P	0.08	3	81	324	70	281
Verbascum thapsus[1]*	D	0.11	3	102	407	229	915
	M	0.11	4	89	356	379	1518
	P	0.41	1	58	229	50	198

[1]Forb; [2]Graminoid; [3]Shrub *Non-native

Table 5. Mean (+ 1 SE) sample size (number of plots or transects) and time-to-sample (hr) required for estimation of mean cover within 50% and 25% of the observed mean cover (90% confidence) for common (n=7) and less-common (n=17) species for each sampling design: Daubenmire transect (D); modified Whittaker plot (M); and point line intercept transect, (P).

	Sample size (#)		Sampling time (hr)	
Sampling design	50%	25%	50%	25%
Common species				
D	9 (1)	32 (4)	19 (2)	71 (8)
M	8 (1)	28 (5)	31 (5)	119 (21)
P	14 (4)	54 (16)	12 (3)	46 (14)
Less-common species				
D	118 (16)	468 (63)	264 (36)	1051 (142)
M	62 (7)	251 (25)	246 (32)	1006 (120)
P	75 (16)	254 (57)	61 (14)	209 (50)

Figure 1. The four sampling designs tested.



Figures from: a. Lutes 2006, b. Abrahamson (unpublished) c. Barnett and Stohlgren 2003 d. modified from Thompson 1991

Figure 2. Location of sampling units within each treatment, including seven modified Whittaker plots established for the FFS study (grey shading), one additional modified Whittaker plot (white shading) for determining installation time, and 16 (dashed) for Daubenmire, point line intercept, and strip adaptive cluster sampling transects.

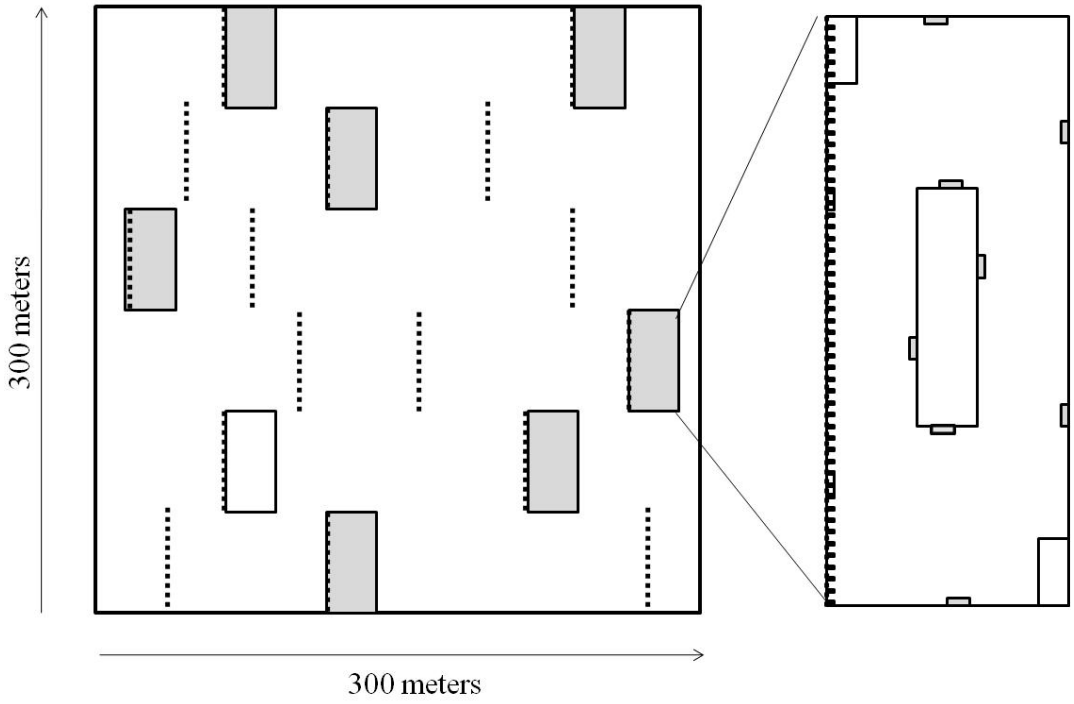


Figure 3. Between-environment (control versus thinned and burned) differences in mean cover (+ 1 SE) (black shading) and within-stand standard deviations (+ 1 SE) (grey shading) for (a) canopy cover, and (b) bare ground.

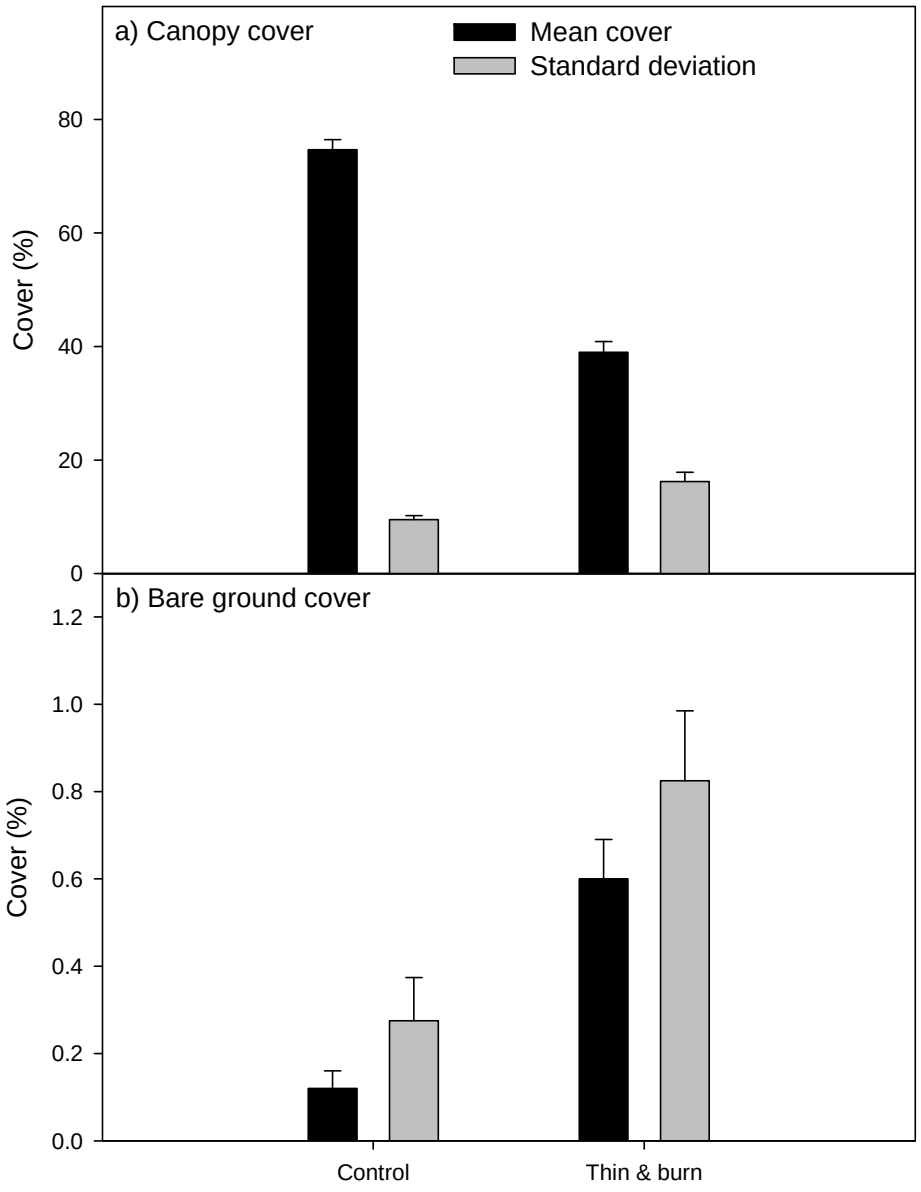


Figure 4. Percent cover (a and b) and within-stand standard deviation (c and d) for grouped vegetation variables by sampling design (Daubenmire transect, closed circle; modified Whittaker 1-m^2 subplots, open circle; and point line intercept transect, closed triangle). Total vegetation includes all species; the other grouped vegetation variables only include the relevant species of the 24 sampled (see *Methods*). Statistical differences in cover among designs were not assessed (see *Methods*). *P*-values from tests for differences in standard deviation among designs are: forbs F=78.66, p<0.001; graminoids F=1060.0, p<0.001; shrubs F=21.95, p=0.001; total vegetation F= 2.58, p=0.003; non-native vegetation F= 3.129, p=0.184; and native vegetation F=27.59, p<0.001.

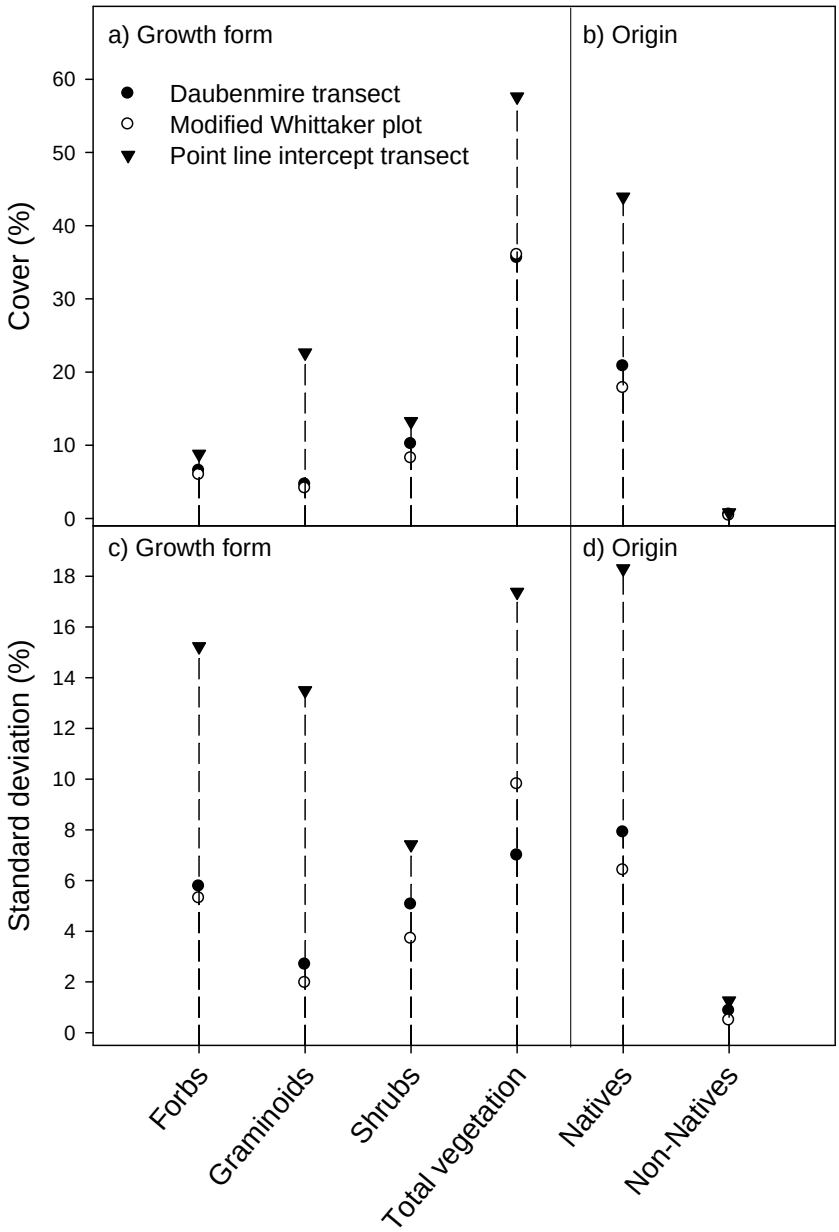


Figure 5. Percent cover (a) and within-stand standard deviation (b) for individual species by sampling design (Daubenmire transect, closed circle; modified Whittaker 1-m^2 subplots, open circle; point line intercept transect, closed triangle; and strip adaptive cluster sampling, open triangle). Statistical differences in cover among designs were not assessed (see *Methods*). *P*-values from tests for differences in standard deviation among designs are: *Arnica cordifolia* F=13.23, p=0.003; *Calamagrostis rubescens* F=233.35, p< 0.001, *Carex geyeri* F=71.75, p<0.001; *Fragaria virginiana* F=12.33, p=0.004; *Mahonia repens* F=16.31. p=0.003; *Penstamon alberti* F=11.51, p=0.004; and *Symphoricarpos albus* F=11.47, p=0.004.

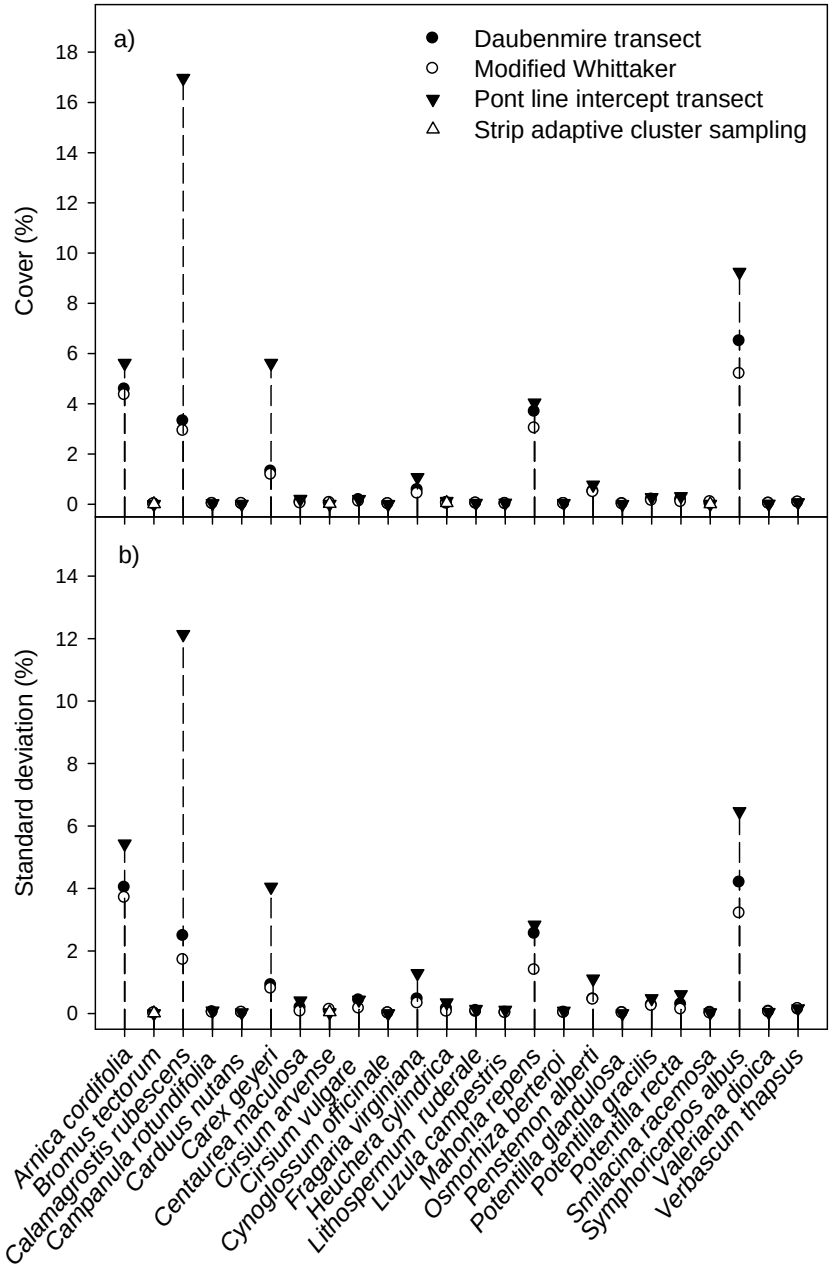


Figure 6. Percent cover (a), within-stand standard deviation (b), and coefficient of variation (c) for the four species sampled using strip adaptive cluster sampling (black shading) in addition to the three multi-species designs (Daubenmire transects, grey shading; modified Whittaker plots, white shading; and point line intercept transects, striped). Coefficient of variations for *Bromus tectorum* and *Cirsium arvense* are based only on data from the thinned and burned stands; they were absent or present on only one control stand.

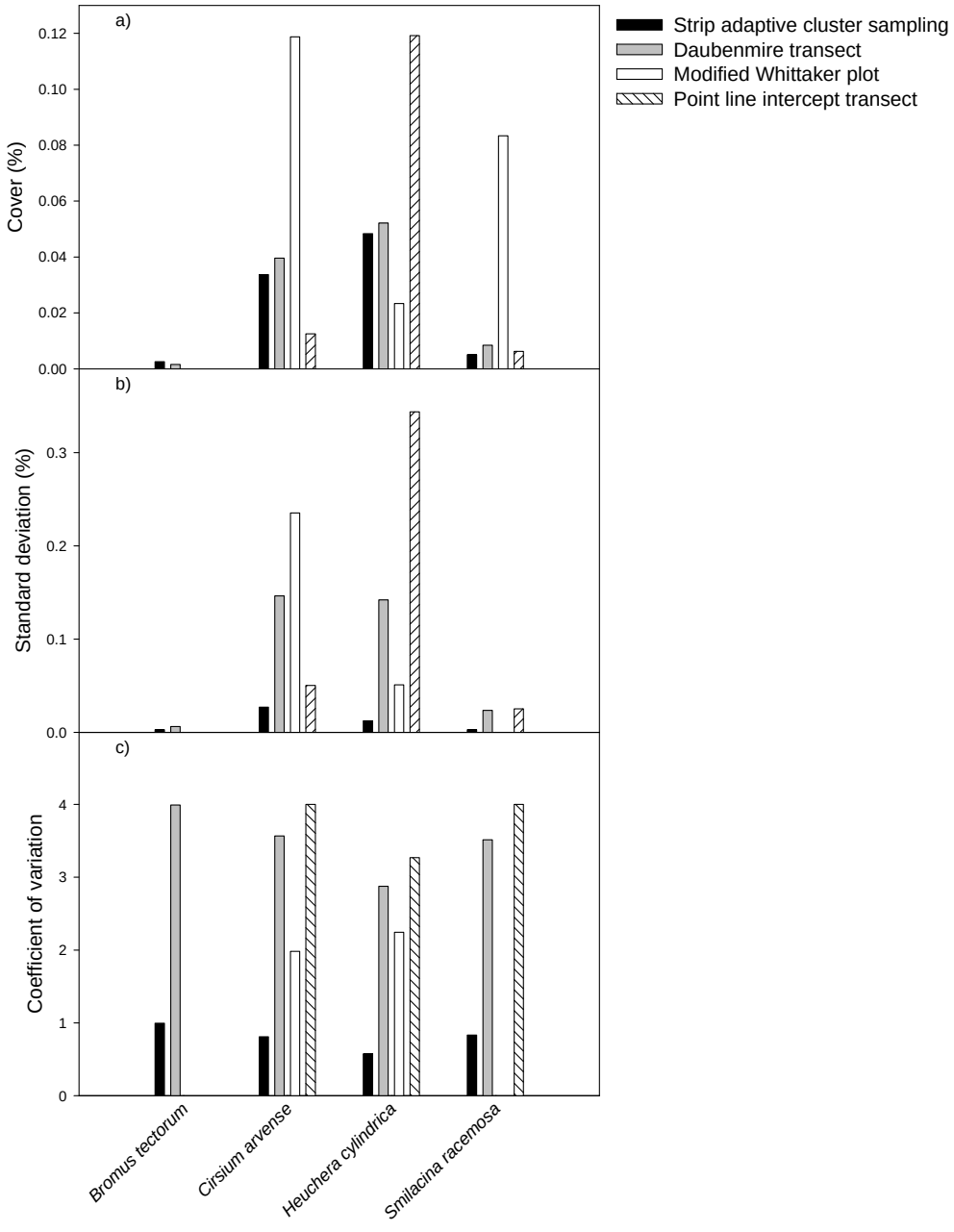


Figure 7. For each of the 24 focal species, mean within-stand frequency (percentage of transects or plots within a stand containing the focal species) for each sampling design (Daubenmire transect, closed circle; modified Whittaker full 1000-m^2 plot, open circle; and point line intercept transect, closed triangle).

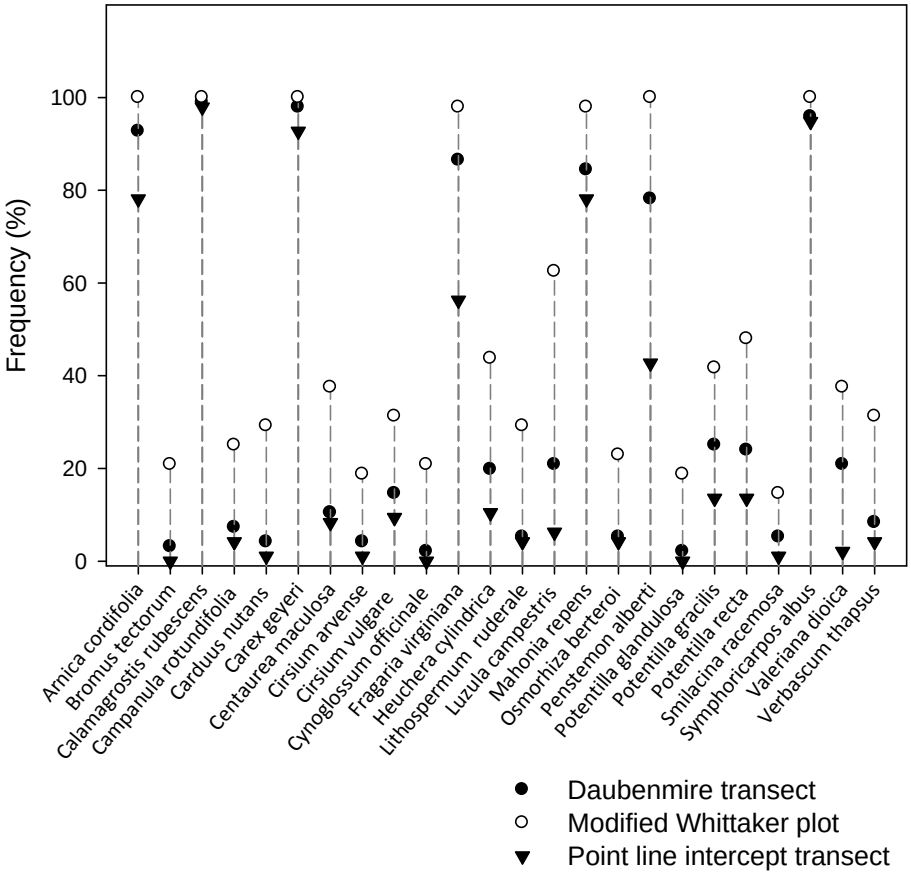


Figure 8. Mean (+ 1 SE) constancy (number of stands in which species was detected) of less-common species for each sampling design (Modified Whittaker 1000-m^2 plots, white shading; modified Whittaker 100-m^2 subplots, coarse horizontal lines; modified Whittaker 10-m^2 subplots, fine horizontal lines; modified Whittaker 1-m^2 subplots, hash marks; Daubenmire transects, black shading; and point line intercept transects, grey shading).

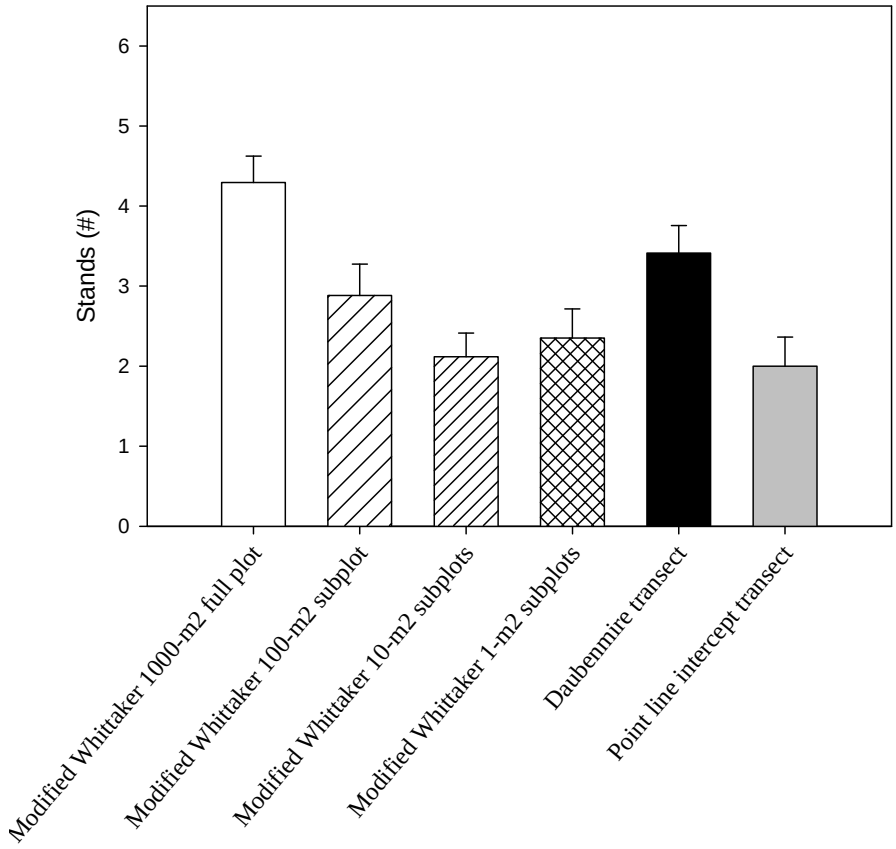


Figure 9. Sample size (a-c) and time (d-f) required to estimate cover of total vegetation (a, d), graminoids (b, e), and non-native plants (c, f) for each sampling design: Daubenmire transect, solid trace; modified Whittaker plot, dotted trace; and point line intercept transect, dashed trace. Open circles indicate 25% relative MoE; solid circles indicate 50% relative MoE. On plot (e), traces for Daubenmire and modified Whittaker designs overlap and can not be visually distinguished.

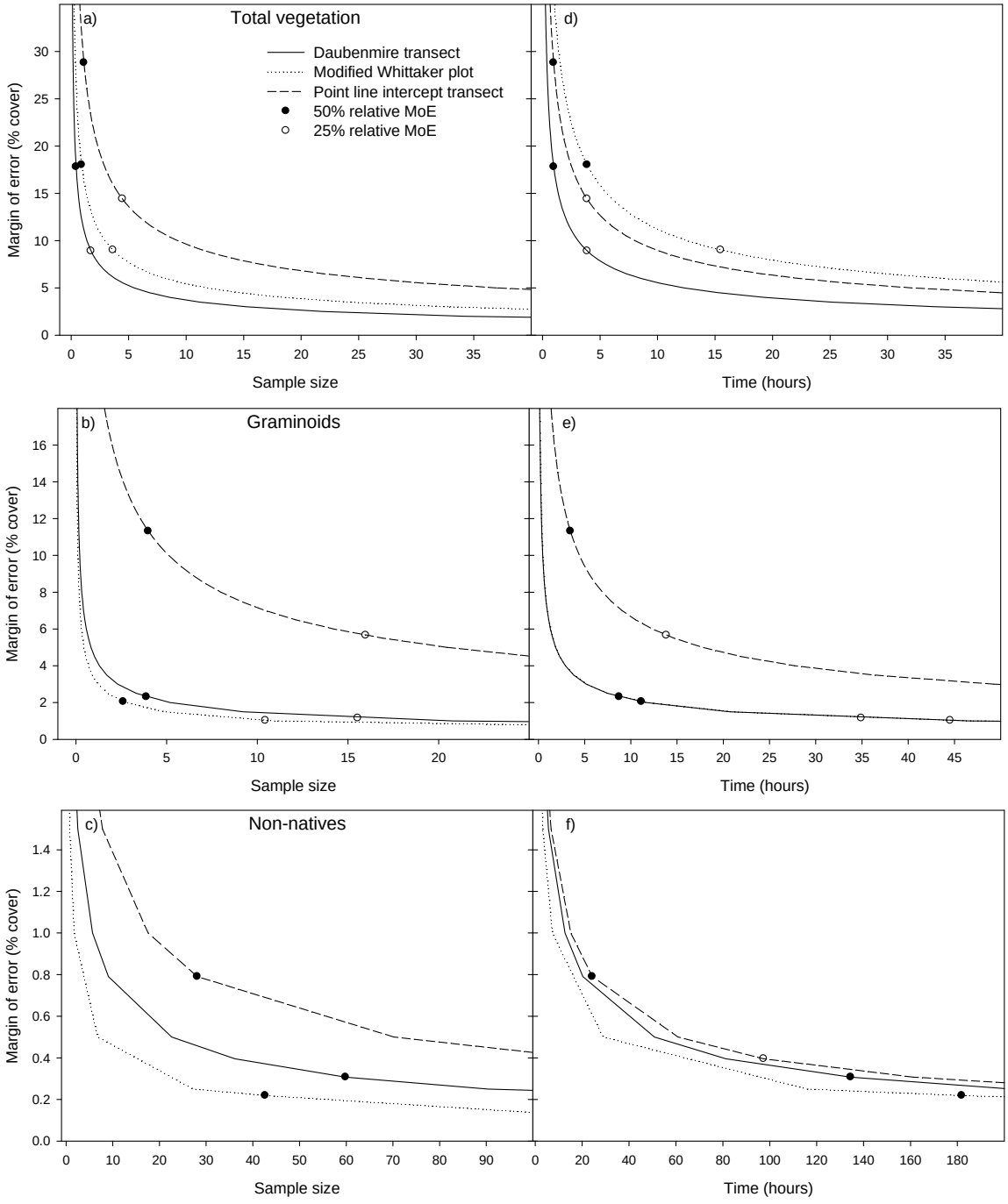
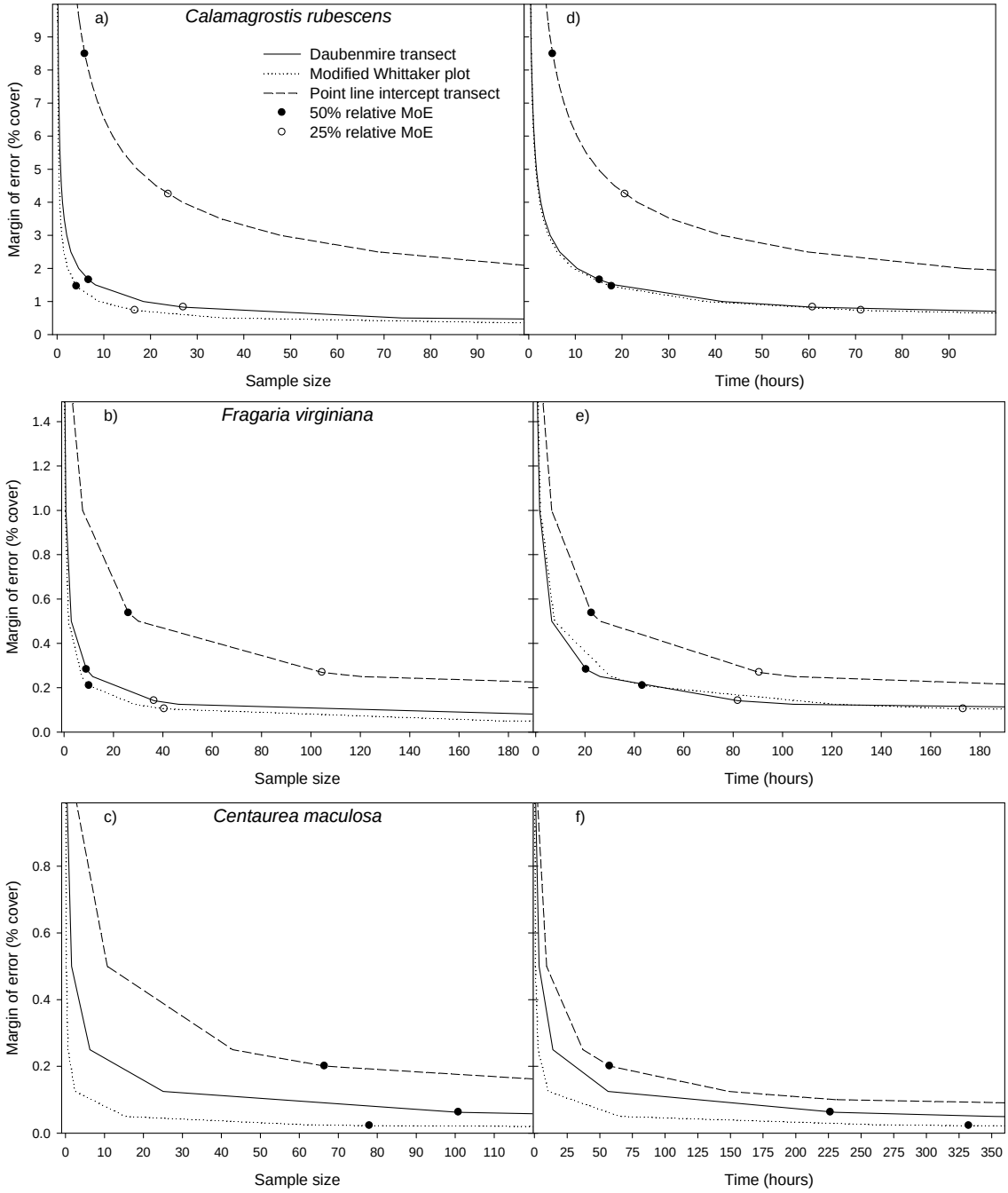


Figure 10**.** Sample size (a-c) and time (d-f) required to estimate percent cover of a common graminoid (*Calamagrostis rubescens*) (a, d), a common, but low-cover forb (*Fragaria virginia*) (b, e), and a less-common non-native forb (*Centaurea maculosa*) (c, f), for each sampling design: Daubenmire transect, solid trace; modified Whittaker plot, dotted trace; point line intercept transect, dashed trace. Open circles indicate 25% relative MoE; solid circles indicate 50% relative MoE. See Table 4 for results for all 24 focal species.



Appendix 1. Constancy (number of stands [0-3] on which a species was detected) and cover (+1 SE) for each species in each environment (control and thinned-and-burned) for each sampling design: Daubenmire transect (D), modified Whittaker plot (M), and point line intercept transect, P). Bold font indicates species that were detected in all three stands by all three designs. Empty cells indicate that the species was not encountered. For cover < 0.005%, *t* indicates trace.

		Control		Thinned and burned	
Species	Design	Constancy (#)	Cover (SE) (%)	Constancy (#)	Cover (SE) (%)
Arnica cordifolia	D	**3**	4.72 (0.4)	**3**	4.43 (1.37)
Arnica cordifolia	M	**3**	4.79 (0.58)	**3**	3.9 (1.48)
Arnica cordifolia	P	**3**	5.6 (0.71)	**3**	5.64 (2.12)
Bromus tectorum	D	1	*t* (*t*)	3	*t* (t)
Bromus tectorum	M	0		0	
Bromus tectorum	P	0		0	
Calamagrostis rubescens	D	**3**	2.29 (0.69)	**3**	4.32 (0.75)
Calamagrostis rubescens	M	**3**	1.98 (0.63)	**3**	3.85 (1)
Calamagrostis rubescens	P	**3**	12.95 (2.86)	**3**	20.98 (5.61)
Campanula rotundifolia	D	2	*t (t)*	3	0.02 (0.01)
Campanula rotundifolia	M	0		1	0.02 (0.02)
Campanula rotundifolia	P	0		2	0.06 (0.05)
Carduus nutans	D	0		2	0.01 (*t*)
Carduus nutans	M	1	*t (t)*	2	0.03 (0.02)
Carduus nutans	P	0		1	0.01 (0.01)
Carex geyeri	D	**3**	1.63 (0.38)	**3**	0.97 (0.13)
Carex geyeri	M	**3**	1.5 (0.47)	**3**	0.85 (0.15)
Carex geyeri	P	**3**	7.05 (1.64)	**3**	4.18 (0.33)
Centaurea maculosa	D	1	0.02 (0.02)	3	0.15 (0.12)
Centaurea maculosa	M	1	0.01 (0.01)	3	0.05 (0.04)
Centaurea maculosa	P	1	0.09 (0.09)	2	0.31 (0.3)
Cirsium arvense	D	0		2	0.04 (0.02)
Cirsium arvense	M	0		1	0.12 (0.12)
Cirsium arvense	P	0		1	0.01 (0.01)

Appendix 1 continued

		Control		Thinned and burned	
Species	Design	Constancy (#)	Cover (SE) (%)	Constancy (#)	Cover (SE) (%)
Cirsium vulgare	D	0		2	0.33 (0.24)
Cirsium vulgare	M	0		2	0.2 (0.11)
Cirsium vulgare	P	0		2	0.39 (0.25)
Cynoglossum officinale	D	0		2	*t* (*t*)
Cynoglossum officinale	M	0		1	*t* (*t*)
Cynoglossum officinale	P	0		0	
Fragaria virginiana	D	**3**	0.32 (0.16)	**3**	0.81 (0.33)
Fragaria virginiana	M	**3**	0.28 (0.14)	**3**	0.56 (0.26)
Fragaria virginiana	P	**3**	0.58 (0.43)	**3**	1.57 (0.66)
Heuchera cylindrica	D	3	0.03 (0.02)	3	0.07 (0.03)
Heuchera cylindrica	M	3	0.02 (0.01)	2	0.02 (0.02)
Heuchera cylindrica	P	2	0.09 (0.07)	3	0.15 (0.06)
Lithospermum ruderale	D	1	0.03 (0.03)	1	0.01 (0.01)
Lithospermum ruderale	M	1	0.03 (0.03)	1	0.03 (0.03)
Lithospermum ruderale	P	1	0.05 (0.05)	1	0.04 (0.04)
Luzula campestris	D	2	0.02 (0.02)	2	0.01 (0.01)
Luzula campestris	M	1	*t* (*t*)	2	0.01 (*t*)
Luzula campestris	P	1	0.05 (0.05)	1	0.05 (0.05)
Mahonia repens	D	**3**	2.92 (1.18)	**3**	4.44 (2.31)
Mahonia repens	M	**3**	2.61 (0.85)	**3**	3.45 (2.25)
Mahonia repens	P	**3**	2.91 (1.04)	**3**	5.16 (2.46)
Osmorhiza berteroi	D	0		1	0.02 (0.02)
Osmorhiza berteroi	M	0		1	0.02 (0.02)
Osmorhiza berteroi	P	0		1	0.08 (0.08)
Penstemon alberti	D	**3**	0.29 (0.11)	**3**	0.72 (0.38)
Penstemon alberti	M	**3**	0.36 (0.12)	**3**	0.6 (0.21)
Penstemon alberti	P	**3**	0.4 (0.14)	**3**	1.13 (0.41)
Potentilla glandulosa	D	0		3	0.02 (0.01)
Potentilla glandulosa	M	0		1	*t* (*t*)
Potentilla glandulosa	P	0		0	
Potentilla gracilis	D	1	0.03 (0.03)	2	0.33 (0.31)
Potentilla gracilis	M	1	0.01 (0.01)	2	0.25 (0.25)
Potentilla gracilis	P	1	0.04 (0.04)	2	0.5 (0.46)

Appendix 1 continued

		Control		Thinned and burned	
Species	Design	Constancy (#)	Cover (SE) (%)	Constancy (#)	Cover (SE) (%)
Potentilla recta	D	1	0.14 (0.14)	2	0.22 (0.2)
Potentilla recta	M	2	0.07 (0.05)	2	0.1 (0.1)
Potentilla recta	P	1	0.3 (0.3)	2	0.33 (0.29)
Smilacina racemosa	D	1	0.01 (0.01)	2	*t* (*t*)
Smilacina racemosa	M	0	0.01 (0.01)	1	0.17 (0.17)
Smilacina racemosa	P	1		0	
Symphoricarpos albus	D	**3**	6.79 (4.08)	**3**	6.19 (1.76)
Symphoricarpos albus	M	**3**	5.72 (2.97)	**3**	4.5 (1.48)
Symphoricarpos albus	P	**3**	9.58 (5.48)	**3**	8.91 (1.8)
Valeriana dioica	D	3	0.02 (*t*)	2	0.04 (0.04)
Valeriana dioica	M	1	0.01 (0.01)	3	0.03 (0.03)
Valeriana dioica	P	0		1	0.03 (0.03)
Verbascum thapsus	D	0		3	0.11 (0.08)
Verbascum thapsus	M	1	*t* (*t*)	3	0.15 (0.11)
Verbascum thapsus	P	0		1	0.14 (0.14)
Total Vegetation Cover	D	**3**	28.84 (2.7)	**3**	42.36 (3.26)
Total Vegetation Cover	M	**3**	28.21 (1.73)	**3**	43.83 (5.03)
Total Vegetation Cover	P	**3**	49.25 (4.17)	**3**	65.96 (9.43)
Forbs	D	**3**	5.67 (0.26)	**3**	7.38 (0.87)
Forbs	M	**3**	5.6 (0.62)	**3**	6.29 (0.72)
Forbs	P	**3**	7.23 (0.66)	**3**	10.39 (2.13)
Graminoids	D	**3**	3.94 (0.36)	**3**	5.31 (0.62)
Graminoids	M	**3**	3.49 (0.37)	**3**	4.7 (0.86)
Graminoids	P	**3**	20.06 (1.51)	**3**	25.21 (5.41)
Shrubs	D	**3**	9.71 (5)	**3**	10.62 (2.17)
Shrubs	M	**3**	8.33 (3.37)	**3**	7.94 (2.39)
Shrubs	P	**3**	12.49 (6.26)	**3**	14.07 (2.19)
Natives	D	**3**	19.15 (4.64)	**3**	22.44 (2.29)
Natives	M	**3**	17.34 (3.44)	**3**	18.28 (2.49)
Natives	P	**3**	39.38 (4.93)	**3**	48.48 (7.22)
Non-Natives	D	2	0.16 (0.16)	3	0.86 (0.43)
Non-Natives	M	2	0.08 (0.05)	3	0.65 (0.41)
Non-Natives	P	1	0.39 (0.39)	2	1.19 (0.63)